

# Genomic Analysis of *Pseudomonas aeruginosa* Resistance to Carbapenem Isolates in Three Major Hospitals in Hanoi (2011-2015)

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**Purpose:** Multidrug-resistant *Pseudomonas aeruginosa* is recognised as an important cause of hospital acquired infections listed among the WHO priority pathogens. The antibiotic resistance mechanisms of *P. aeruginosa* have been well documented. However, antibiotic resistance genes carried by *P. aeruginosa* differ markedly among communities and countries. **Procedure:** Whole genome sequence analysis was used to identify the antibiotic-resistance genes and phylogenetic structure of 72 carbapenem-resistant *P. aeruginosa* isolates from hospital acquired infection patients between 2011-2015 in three major hospitals in Hanoi-Vietnam. **Results:** All of *P. aeruginosa* strains carry different antibiotic resistance genes. Of these 48/72 strains carrying 3 variants of IMP genes, in which IMP-15 gene dominates (n= 34). Two strains were co-carried IMP-15+DIM-1 genes and 7 were positive to KPC-1. High MICs for imipenem may related to IMP-, DIM-1 and KPC-1 genes. Phylogenetic analysis has divided these isolates into 9 groups. Each group harbors characteristic drug resistance genes and genetic background. Sixteen STs, including 8 STs found in Vietnam and other continents; 8 STs only found in Vietnam and 2 novel STs were unidentified. The mobile genetic elements of IMP-51, DIM-1 and KPC-1 genes were similar to other countries in the world. **Conclusions:** These finding suggest high diversity and high proportions of carbapenem resistance among hospital isolates of *P. aeruginosa* and clonal expansion in hospitals associated with selection by antibiotic exposure. Most ST were described before in the region and world-wide suggesting global spread due to the globalization. Co-existence of IMP-15 + DIM-1 and KPC-1 genes in *P. aeruginosa* is first reported Vietnam.